OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/017,086

DATE: 01/03/2002
TIME: 15:37:23

Input Set : A:\Seq__Listing_for_P2630P1C64.wpd
Output Set: N:\CRF3\01032002\J017086.raw

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 3 <110> APPLICANT: Ashkenazi, Avi
 4        Baker Kevin P.
 5        Botstein, David
 6        Desnoyers, Luc
 7        Eaton, Dan
 8        Ferrara, Napoleon
 9        Filvaroff, Ellen
10        Fong, Sherman
11        Gao, Wei-Qiang
12        Gerber, Hanspeter
13        Gerritsen, Mary E.
14        Goddard, Audrey
15        Godowski, Paul J.
16        Grimaldi, J. Christopher
17        Gurney, Austin L.
18        Hillan, Kenneth J
19        Kljavin, Ivar J.
20        Kuo, Sophia S.
21        Napier, Mary A.
22        Pan, James;
23        Paoni, Nicholas F.
24        Roy, Margaret Ann
25        Shelton, David L.
26        Stewart, Timothy A.
27        Tumas, Daniel
28        Williams, P. Mickey
29        Wood, William I.
31 <120> TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
32        Acids Encoding the Same
34 <130> FILE REFERENCE: P2630P1C64
36 <140> CURRENT APPLICATION NUMBER: US/10/017,086
36 <141> CURRENT FILING DATE: 2001-10-24
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Does Not Comply
Corrected Diskette Needed

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RAW SEQUENCE LISTING
PATENT APPLICATION: **US/10/017,086**

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TIME: 15:37:23

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Output Set: **N:\CRF3\01032002\J017086.raw**

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/017,086

DATE: 01/03/2002
TIME: 15:37:23

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Output Set: N:\CRF3\01032002\J017086.raw

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W--> (handwritten) → 1998-05-07 = use this date format — please edit all subsequent date errors

RAW SEQUENCE LISTING   DATE: 01/03/2002
PATENT APPLICATION: US/10/017,086   TIME: 15:37:23

Input Set : A:\Seq__Listing_for_P2630P1C64.wpd
Output Set: N:\CRF3\01032002\J017086.raw

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10/017,086.

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<211> 412
<212> PRT
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see item 11 on Err Summary Sheet

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<400> 157
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Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

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L:36 M:270 C: Current Application Number differs, Replaced Current Application No
L:36 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:244 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:370 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:445 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:978 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:980 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:992 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1012 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
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L:1811 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
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L:4955 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:117
L:5050 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:118
L:5052 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:118
L:5756 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:137
L:5918 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:144
L:5920 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:144
L:6192 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:151
L:6196 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:151
L:6223 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:152
L:6225 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:152
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Input Set : **A:\Seq__Listing_for_P2630P1C64.wpd**
Output Set: **N:\CRF3\01032002\J017086.raw**

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L:6387 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:157
L:6389 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:6389 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:7713 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:191
L:7719 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:191
L:7729 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:191
L:8724 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:215
L:10653 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:265
L:10655 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:265
L:10657 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:265
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ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _10/017,086_
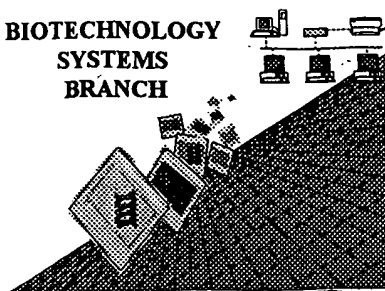
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWAR

1____Wrapped Nucleics
    Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino
    Numbering

The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____Variable Length

Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0
    "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7____Skipped Sequences
    (OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences
    (NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's
    (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213>
    Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11____Use of <220>

Sequence(s) _157_ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0
    "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY SYSTEMS BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/017,086_
Source: _O1PE_
Date Processed by STIC: _1/3/2002_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: **patin21help@uspto.gov** or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: **patin3help@uspto.gov** or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:
1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry** directly to:
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          Or
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